

SEQUENCE LISTING

<110> Brumbley, Stevens Michael  
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<120> TRANSGENIC PLANTS USED AS A BIOREACTOR SYSTEM

<130> 900145.403USPC

<140> US 10/520,882

<141> 2003-07-11

<150> PCT/AU2003/000903

<151> 2003-07-11

<150> US 60/394,869

<151> 2002-07-11

<160> 56

<170> PatentIn version 3.0

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<211> 1182

<212> DNA

<213> Rastonia Eutropia

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Pro	Ala	Arg	Gln	Ala	Ala	Ile	Lys	Ala	Gly	Leu	Pro	Ala	Met	Val	Pro	
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Gly	Gly	Gln	Glu	Asn	Met	Ser	Ala	Ala	Pro	His	Val	Leu	Pro	Gly	Ser	
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Arg	Asp	Gly	Phe	Arg	Met	Gly	Asp	Ala	Lys	Leu	Val	Asp	Thr	Met	Ile	
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Glu	Phe	Ala	Val	Gly	Ser	Gln	Asn	Lys	Ala	Glu	Ala	Ala	Gln	Lys	Ala	
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Lys Val Asn Val Asn Gly Gly Ala Ile Ala Ile Gly His Pro Ile Gly	
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Ala Ser Gly Cys Arg Ile Leu Val Thr Leu Leu His Glu Met Lys Arg	
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Arg Asp Ala Lys Lys Gly Leu Ala Ser Leu Cys Ile Gly Gly Gly Met	
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&lt;212&gt; PRT

&lt;213&gt; Rastonia Eutropia

&lt;400&gt; 2

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Ser Glu Val Ile Met Gly Gln Val Leu Thr Ala Gly Ser Gly Gln Asn  
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Ala Met Thr Ile Asn Lys Val Cys Gly Ser Gly Leu Lys Ala Val Met  
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Glu Phe Ala Val Gly Ser Gln Asn Lys Ala Glu Ala Ala Gln Lys Ala  
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Gly Lys Phe Asp Glu Glu Ile Val Pro Val Leu Ile Pro Gln Arg Lys  
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Gly Asp Pro Val Ala Phe Lys Thr Asp Glu Phe Val Arg Gln Gly Ala  
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Glu Trp Thr Pro Gln Asp Leu Asp Leu Met Glu Ile Asn Glu Ala Phe  
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Ala Ser Gly Cys Arg Ile Leu Val Thr Leu Leu His Glu Met Lys Arg  
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&lt;222&gt; (1)..(738)

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85 90 95	
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Asp Arg Gly Trp Gly Arg Ile Val Asn Ile Ser Ser Val Asn Gly Gln	
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&lt;212&gt; PRT

&lt;213&gt; Rastonia Eutropia

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Gly	Cys	Gly	Pro	Asn	Ser	Pro	Arg	Arg	Glu	Lys	Trp	Leu	Glu	Gln	Gln	
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Lys	Ala	Leu	Gly	Phe	Asp	Phe	Ile	Ala	Ser	Glu	Gly	Asn	Val	Ala	Asp	
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Trp Asp Ser Thr Lys Thr Ala Phe Asp Lys Val Lys Ser Glu Val Gly  
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Glu Val Asp Val Leu Ile Asn Asn Ala Gly Ile Thr Arg Asp Val Val  
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Phe Arg Lys Met Thr Arg Ala Asp Trp Asp Ala Val Ile Asp Thr Asn  
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Leu Thr Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp Gly Met Ala  
115 120 125

Asp Arg Gly Trp Gly Arg Ile Val Asn Ile Ser Ser Val Asn Gly Gln  
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Lys Gly Gln Phe Gly Gln Thr Asn Tyr Ser Thr Ala Lys Ala Gly Leu  
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His Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Thr Lys Gly Val  
165 170 175

Thr Val Asn Thr Val Ser Pro Gly Tyr Ile Ala Thr Asp Met Val Lys  
180 185 190

Ala Ile Arg Gln Asp Val Leu Asp Lys Ile Val Ala Thr Ile Pro Val  
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Glu Trp Ser Arg Gln Trp Gln Gly Thr Glu Gly Asn Gly His Ala Ala	
35 40 45	
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Ala Ser Gly Ile Pro Gly Leu Asp Ala Leu Ala Gly Val Lys Ile Ala	
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ccg gcg cag ctg ggt gat atc cag cag cgc tac atg aag gac ttc tca	240
Pro Ala Gln Leu Gly Asp Ile Gln Gln Arg Tyr Met Lys Asp Phe Ser	
65 70 75 80	
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Ala Leu Trp Gln Ala Met Ala Glu Gly Lys Ala Glu Ala Thr Gly Pro	
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Leu His Asp Arg Arg Phe Ala Gly Asp Ala Trp Arg Thr Asn Leu Pro	
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Tyr Arg Phe Ala Ala Ala Phe Tyr Leu Leu Asn Ala Arg Ala Leu Thr	
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Glu Leu Ala Asp Ala Val Glu Ala Asp Ala Lys Thr Arg Gln Arg Ile	
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Arg Phe Ala Ile Ser Gln Trp Val Asp Ala Met Ser Pro Ala Asn Phe	
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ctt gcc acc aat ccc gag gcg cag cgc ctg ctg atc gag tcg ggc ggc	528
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Glu Ser Leu Arg Ala Gly Val Arg Asn Met Met Glu Asp Leu Thr Arg	
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ggc aag atc tcg cag acc gac gag agc gcg ttt gag gtc ggc cgc aat	624
Gly Lys Ile Ser Gln Thr Asp Glu Ser Ala Phe Glu Val Gly Arg Asn	
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Glu	His	Pro	Ala	Ala	Ser	Val	Thr	Leu	Leu	Thr	Thr	Leu	Leu	Asp	Phe	
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ttg	cg	gag	gcc	acg	ctg	ggc	ggc	ggc	gcc	ggc	gcg	ccg	tgc	gcg	ctg	1152
Leu	Arg	Glu	Ala	Thr	Leu	Gly	Gly	Gly	Ala	Gly	Ala	Pro	Cys	Ala	Leu	
	370					375					380					
ctg	cg	ggc	ctt	gag	ctg	gcc	aat	acc	ttc	tgc	ttc	ttg	cg	ccg	aac	1200
Leu	Arg	Gly	Leu	Glu	Leu	Ala	Asn	Thr	Phe	Ser	Phe	Leu	Arg	Pro	Asn	
385					390					395					400	
gac	ctg	gtg	tgg	aac	tac	gtg	gtc	gac	aac	tac	ctg	aag	ggc	aac	acg	1248
Asp	Leu	Val	Trp	Asn	Tyr	Val	Val	Asp	Asn	Tyr	Leu	Lys	Gly	Asn	Thr	
				405					410					415		
ccg	gtg	ccg	ttc	gac	ctg	ctg	ttc	tgg	aac	ggc	gac	gcc	acc	aac	ctg	1296
Pro	Val	Pro	Phe	Asp	Leu	Leu	Phe	Trp	Asn	Gly	Asp	Ala	Thr	Asn	Leu	
			420					425					430			

ccg ggg ccg tgg tac tgc tgg tac ctg cgc cac acc tac ctg cag aac	1344
Pro Gly Pro Trp Tyr Cys Trp Tyr Leu Arg His Thr Tyr Leu Gln Asn	
435 440 445	
gag ctc aag gta ccg ggc aag ctg acc gtg tgc ggc gtg ccg gtg gac	1392
Glu Leu Lys Val Pro Gly Lys Leu Thr Val Cys Gly Val Pro Val Asp	
450 455 460	
ctg gcc agc atc gac gtg ccg acc tat atc tac ggc tcg cgc gaa gac	1440
Leu Ala Ser Ile Asp Val Pro Thr Tyr Ile Tyr Gly Ser Arg Glu Asp	
465 470 475 480	
cat atc gtg ccg tgg acc gcg gcc tat gcc tcg acc gcg ctg ctg gcg	1488
His Ile Val Pro Trp Thr Ala Ala Tyr Ala Ser Thr Ala Leu Leu Ala	
485 490 495	
aac aag ctg cgc ttc gtg ctg ggt gcg tcg ggc cat atc gcc ggt gtg	1536
Asn Lys Leu Arg Phe Val Leu Gly Ala Ser Gly His Ile Ala Gly Val	
500 505 510	
atc aac ccg ccg gcc aag aac aag cgc agc cac tgg act aac gat gcg	1584
Ile Asn Pro Pro Ala Lys Asn Lys Arg Ser His Trp Thr Asn Asp Ala	
515 520 525	
ctg ccg gag tcg ccg cag caa tgg ctg gcc ggc gcc atc gag cat cac	1632
Leu Pro Glu Ser Pro Gln Gln Trp Leu Ala Gly Ala Ile Glu His His	
530 535 540	
ggc agc tgg tgg ccg gac tgg acc gca tgg ctg gcc ggg cag gcc ggc	1680
Gly Ser Trp Trp Pro Asp Trp Thr Ala Trp Leu Ala Gly Gln Ala Gly	
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gcg aaa cgc gcc gcg ccc gcc aac tat gcc aat gcg cgc tat cgc gca	1728
Ala Lys Arg Ala Ala Pro Ala Asn Tyr Gly Asn Ala Arg Tyr Arg Ala	
565 570 575	
atc gaa ccc gcg cct ggg cga tac gtc aaa gcc aag gca	1767
Ile Glu Pro Ala Pro Gly Arg Tyr Val Lys Ala Lys Ala	
580 585	

&lt;210&gt; 8

&lt;211&gt; 589

&lt;212&gt; PRT

&lt;213&gt; Rastonia Eutropia

&lt;400&gt; 8

Met Ala Thr Gly Lys Gly Ala Ala Ala Ser Thr Gln Glu Gly Lys Ser  
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 Gln Pro Phe Lys Val Thr Pro Gly Pro Phe Asp Pro Ala Thr Trp Leu  
 20 25 30  
 Glu Trp Ser Arg Gln Trp Gln Gly Thr Glu Gly Asn Gly His Ala Ala  
 35 40 45  
 Ala Ser Gly Ile Pro Gly Leu Asp Ala Leu Ala Gly Val Lys Ile Ala  
 50 55 60  
 Pro Ala Gln Leu Gly Asp Ile Gln Gln Arg Tyr Met Lys Asp Phe Ser  
 65 70 75 80  
 Ala Leu Trp Gln Ala Met Ala Glu Gly Lys Ala Glu Ala Thr Gly Pro  
 85 90 95  
 Leu His Asp Arg Arg Phe Ala Gly Asp Ala Trp Arg Thr Asn Leu Pro  
 100 105 110  
 Tyr Arg Phe Ala Ala Ala Phe Tyr Leu Leu Asn Ala Arg Ala Leu Thr  
 115 120 125  
 Glu Leu Ala Asp Ala Val Glu Ala Asp Ala Lys Thr Arg Gln Arg Ile  
 130 135 140  
 Arg Phe Ala Ile Ser Gln Trp Val Asp Ala Met Ser Pro Ala Asn Phe  
 145 150 155 160  
 Leu Ala Thr Asn Pro Glu Ala Gln Arg Leu Leu Ile Glu Ser Gly Gly  
 165 170 175  
 Glu Ser Leu Arg Ala Gly Val Arg Asn Met Met Glu Asp Leu Thr Arg  
 180 185 190  
 Gly Lys Ile Ser Gln Thr Asp Glu Ser Ala Phe Glu Val Gly Arg Asn  
 195 200 205  
 Val Ala Val Thr Glu Gly Ala Val Val Phe Glu Asn Glu Tyr Phe Gln  
 210 215 220

Leu Leu Gln Tyr Lys Pro Leu Thr Asp Lys Val His Ala Arg Pro Leu  
 225 230 235 240

Leu Met Val Pro Pro Cys Ile Asn Lys Tyr Tyr Ile Leu Asp Leu Gln  
 245 250 255

Pro Glu Ser Ser Leu Val Arg His Val Val Glu Gln Gly His Thr Val  
 260 265 270

Phe Leu Val Ser Trp Arg Asn Pro Asp Ala Ser Met Ala Gly Ser Thr  
 275 280 285

Trp Asp Asp Tyr Ile Glu His Ala Ala Ile Arg Ala Ile Glu Val Ala  
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Arg Asp Ile Ser Gly Gln Asp Lys Ile Asn Val Leu Gly Phe Cys Val  
 305 310 315 320

Gly Gly Thr Ile Val Ser Thr Ala Leu Ala Val Leu Ala Ala Arg Gly  
 325 330 335

Glu His Pro Ala Ala Ser Val Thr Leu Leu Thr Thr Leu Leu Asp Phe  
 340 345 350

Ala Asp Thr Gly Ile Leu Asp Val Phe Val Asp Glu Gly His Val Gln  
 355 360 365

Leu Arg Glu Ala Thr Leu Gly Gly Gly Ala Gly Ala Pro Cys Ala Leu  
 370 375 380

Leu Arg Gly Leu Glu Leu Ala Asn Thr Phe Ser Phe Leu Arg Pro Asn  
 385 390 395 400

Asp Leu Val Trp Asn Tyr Val Val Asp Asn Tyr Leu Lys Gly Asn Thr  
 405 410 415

Pro Val Pro Phe Asp Leu Leu Phe Trp Asn Gly Asp Ala Thr Asn Leu  
 420 425 430

Pro Gly Pro Trp Tyr Cys Trp Tyr Leu Arg His Thr Tyr Leu Gln Asn  
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Glu Leu Lys Val Pro Gly Lys Leu Thr Val Cys Gly Val Pro Val Asp  
 450 455 460

Leu Ala Ser Ile Asp Val Pro Thr Tyr Ile Tyr Gly Ser Arg Glu Asp  
 465 470 475 480

His Ile Val Pro Trp Thr Ala Ala Tyr Ala Ser Thr Ala Leu Leu Ala  
 485 490 495

Asn Lys Leu Arg Phe Val Leu Gly Ala Ser Gly His Ile Ala Gly Val  
 500 505 510

Ile Asn Pro Pro Ala Lys Asn Lys Arg Ser His Trp Thr Asn Asp Ala  
 515 520 525

Leu Pro Glu Ser Pro Gln Gln Trp Leu Ala Gly Ala Ile Glu His His  
 530 535 540

Gly Ser Trp Trp Pro Asp Trp Thr Ala Trp Leu Ala Gly Gln Ala Gly  
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Ala Lys Arg Ala Ala Pro Ala Asn Tyr Gly Asn Ala Arg Tyr Arg Ala  
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Ile Glu Pro Ala Pro Gly Arg Tyr Val Lys Ala Lys Ala  
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<210> 9

<211> 1800

<212> DNA

<213> Rastonia Eutropia

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gaccggcgct tcgccggcga cgcattggcg accaacctcc catatcgctt cgctgccgcg	360
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gacgagagcg cgtttgaggt cggccgcaat gtcgcggtga ccgaaggcg cgtggtcttc	660
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gccggcgcgga aacgcgcgcg gcccgccaac tatggcaatg cgcgctatcg cgcaatcgaa	1740

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<210> 10

<211> 1428

<212> DNA

<213> Rastonia Eutropia

<220>

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<400> 10

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tct agg ggg caa tcc gcc gca atg gct cca ttc ggc ggc ctc aaa tcc	96
Ser Arg Gly Gln Ser Ala Ala Met Ala Pro Phe Gly Gly Leu Lys Ser	
20 25 30	

atg act gga ttc cca gtg aag aag gtc aac act gac att act tcc att	144
Met Thr Gly Phe Pro Val Lys Lys Val Asn Thr Asp Ile Thr Ser Ile	
35 40 45	

aca agc aat ggt gga aga gta aag tgc atg cag gtg tgg cct cca att	192
Thr Ser Asn Gly Gly Arg Val Lys Cys Met Gln Val Trp Pro Pro Ile	
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gga aag aag aag ttt gag act ctt tcc tat ttg cca cca ttg acc aga	240
Gly Lys Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg	
65 70 75 80	

gat tcc cgg gtg act gac gtt gtc atc gta tcc gcc gcc cgc acc gcg	288
Asp Ser Arg Val Thr Asp Val Val Ile Val Ser Ala Ala Arg Thr Ala	
85 90 95	

gtc ggc aag ttt ggc ggc tcg ctg gcc aag atc ccg gca ccg gaa ctg	336
Val Gly Lys Phe Gly Gly Ser Leu Ala Lys Ile Pro Ala Pro Glu Leu	
100 105 110	

ggg gcc gtg gtc atc aag gcc gcg ctg gag cgc gcc ggc gtc aag ccg	384
Gly Ala Val Val Ile Lys Ala Ala Leu Glu Arg Ala Gly Val Lys Pro	
115 120 125	

gag	cag	gtg	agc	gaa	gtc	atc	atg	ggc	cag	gtg	ctg	acc	gcc	ggg	tcg	432
Glu	Gln	Val	Ser	Glu	Val	Ile	Met	Gly	Gln	Val	Leu	Thr	Ala	Gly	Ser	
	130					135					140					
ggc	cag	aac	ccc	gca	cgc	cag	gcc	gcg	atc	aag	gcc	ggc	ctg	ccg	gcg	480
Gly	Gln	Asn	Pro	Ala	Arg	Gln	Ala	Ala	Ile	Lys	Ala	Gly	Leu	Pro	Ala	
145					150					155					160	
atg	gtg	ccg	gcc	atg	acc	atc	aac	aag	gtg	tgc	ggc	tcg	ggc	ctg	aag	528
Met	Val	Pro	Ala	Met	Thr	Ile	Asn	Lys	Val	Cys	Gly	Ser	Gly	Leu	Lys	
				165					170					175		
gcc	gtg	atg	ctg	gcc	gcc	aac	gcg	atc	atg	gcg	ggc	gac	gcc	gag	atc	576
Ala	Val	Met	Leu	Ala	Ala	Asn	Ala	Ile	Met	Ala	Gly	Asp	Ala	Glu	Ile	
			180					185					190			
gtg	gtg	gcc	ggc	ggc	cag	gaa	aac	atg	agc	gcc	gcc	ccg	cac	gtg	ctg	624
Val	Val	Ala	Gly	Gly	Gln	Glu	Asn	Met	Ser	Ala	Ala	Pro	His	Val	Leu	
		195					200					205				
ccg	ggc	tcg	cgc	gat	ggg	ttc	cgc	atg	ggc	gat	gcc	aag	ctg	gtc	gac	672
Pro	Gly	Ser	Arg	Asp	Gly	Phe	Arg	Met	Gly	Asp	Ala	Lys	Leu	Val	Asp	
	210					215					220					
acc	atg	atc	gtc	gac	ggc	ctg	tgg	gac	gtg	tac	aac	cag	tac	cac	atg	720
Thr	Met	Ile	Val	Asp	Gly	Leu	Trp	Asp	Val	Tyr	Asn	Gln	Tyr	His	Met	
225					230					235					240	
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Gly	Ile	Thr	Ala	Glu	Asn	Val	Ala	Lys	Glu	Tyr	Gly	Ile	Thr	Arg	Glu	
				245					250					255		
gcg	cag	gat	gag	ttc	gcc	gtc	ggc	tcg	cag	aac	aag	gcc	gaa	gcc	gcg	816
Ala	Gln	Asp	Glu	Phe	Ala	Val	Gly	Ser	Gln	Asn	Lys	Ala	Glu	Ala	Ala	
			260					265					270			
cag	aag	gcc	ggc	aag	ttt	gac	gaa	gag	atc	gtc	ccg	gtg	ctg	atc	ccg	864
Gln	Lys	Ala	Gly	Lys	Phe	Asp	Glu	Glu	Ile	Val	Pro	Val	Leu	Ile	Pro	
		275					280					285				
cag	cgc	aag	ggc	gac	ccg	gtg	gcc	ttc	aag	acc	gac	gag	ttc	gtg	cgc	912
Gln	Arg	Lys	Gly	Asp	Pro	Val	Ala	Phe	Lys	Thr	Asp	Glu	Phe	Val	Arg	
	290					295					300					
cag	ggc	gcc	acg	ctg	gac	agc	atg	tcc	ggc	ctc	aag	ccc	gcc	ttc	gac	960
Gln	Gly	Ala	Thr	Leu	Asp	Ser	Met	Ser	Gly	Leu	Lys	Pro	Ala	Phe	Asp	
305					310					315					320	
aag	gcc	ggc	acg	gtg	acc	gcg	gcc	aac	gcc	tcg	ggc	ctg	aac	gac	ggc	1008
Lys	Ala	Gly	Thr	Val	Thr	Ala	Ala	Asn	Ala	Ser	Gly	Leu	Asn	Asp	Gly	
				325					330					335		
gcc	gcc	gcg	gtg	gtg	gtg	atg	tcg	gcg	gcc	aag	gcc	aag	gaa	ctg	ggc	1056

Ala	Ala	Ala	Val	Val	Val	Met	Ser	Ala	Ala	Lys	Ala	Lys	Glu	Leu	Gly		
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ctg	acc	ccg	ctg	gcc	acg	atc	aag	agc	tat	gcc	aac	gcc	ggt	gtc	gat	1104	
Leu	Thr	Pro	Leu	Ala	Thr	Ile	Lys	Ser	Tyr	Ala	Asn	Ala	Gly	Val	Asp		
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ccc	aag	gtg	atg	ggc	atg	ggc	ccg	gtg	ccg	gcc	tcc	aag	cgc	gcc	ctg	1152	
Pro	Lys	Val	Met	Gly	Met	Gly	Pro	Val	Pro	Ala	Ser	Lys	Arg	Ala	Leu		
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Ser	Arg	Ala	Glu	Trp	Thr	Pro	Gln	Asp	Leu	Asp	Leu	Met	Glu	Ile	Asn		
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Glu	Ala	Phe	Ala	Ala	Gln	Ala	Leu	Ala	Val	His	Gln	Gln	Met	Gly	Trp		
			405					410						415			
gac	acc	tcc	aag	gtc	aat	gtg	aac	ggc	ggc	gcc	atc	gcc	atc	ggc	cac	1296	
Asp	Thr	Ser	Lys	Val	Asn	Val	Asn	Gly	Gly	Ala	Ile	Ala	Ile	Gly	His		
			420					425					430				
ccg	atc	ggc	gcg	tcg	ggc	tgc	cgt	atc	ctg	gtg	acg	ctg	ctg	cac	gag	1344	
Pro	Ile	Gly	Ala	Ser	Gly	Cys	Arg	Ile	Leu	Val	Thr	Leu	Leu	His	Glu		
		435					440					445					
atg	aag	cgc	cgt	gac	gcg	aag	aag	ggc	ctg	gcc	tcg	ctg	tgc	atc	ggc	1392	
Met	Lys	Arg	Arg	Asp	Ala	Lys	Lys	Gly	Leu	Ala	Ser	Leu	Cys	Ile	Gly		
		450				455					460						
ggc	ggc	atg	ggc	gtg	gcg	ctg	gca	gtc	gag	cgc	aaa					1428	
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&lt;210&gt; 11

&lt;211&gt; 476

&lt;212&gt; PRT

&lt;213&gt; Rastonia Eutropia

&lt;400&gt; 11

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		20						25					30		

Met	Thr	Gly	Phe	Pro	Val	Lys	Lys	Val	Asn	Thr	Asp	Ile	Thr	Ser	Ile	35	40	45	
Thr	Ser	Asn	Gly	Gly	Arg	Val	Lys	Cys	Met	Gln	Val	Trp	Pro	Pro	Ile	50	55	60	
Gly	Lys	Lys	Lys	Phe	Glu	Thr	Leu	Ser	Tyr	Leu	Pro	Pro	Leu	Thr	Arg	65	70	75	80
Asp	Ser	Arg	Val	Thr	Asp	Val	Val	Ile	Val	Ser	Ala	Ala	Arg	Thr	Ala	85	90	95	
Val	Gly	Lys	Phe	Gly	Gly	Ser	Leu	Ala	Lys	Ile	Pro	Ala	Pro	Glu	Leu	100	105	110	
Gly	Ala	Val	Val	Ile	Lys	Ala	Ala	Leu	Glu	Arg	Ala	Gly	Val	Lys	Pro	115	120	125	
Glu	Gln	Val	Ser	Glu	Val	Ile	Met	Gly	Gln	Val	Leu	Thr	Ala	Gly	Ser	130	135	140	
Gly	Gln	Asn	Pro	Ala	Arg	Gln	Ala	Ala	Ile	Lys	Ala	Gly	Leu	Pro	Ala	145	150	155	160
Met	Val	Pro	Ala	Met	Thr	Ile	Asn	Lys	Val	Cys	Gly	Ser	Gly	Leu	Lys	165	170	175	
Ala	Val	Met	Leu	Ala	Ala	Asn	Ala	Ile	Met	Ala	Gly	Asp	Ala	Glu	Ile	180	185	190	
Val	Val	Ala	Gly	Gly	Gln	Glu	Asn	Met	Ser	Ala	Ala	Pro	His	Val	Leu	195	200	205	
Pro	Gly	Ser	Arg	Asp	Gly	Phe	Arg	Met	Gly	Asp	Ala	Lys	Leu	Val	Asp	210	215	220	
Thr	Met	Ile	Val	Asp	Gly	Leu	Trp	Asp	Val	Tyr	Asn	Gln	Tyr	His	Met	225	230	235	240

Gly Ile Thr Ala Glu Asn Val Ala Lys Glu Tyr Gly Ile Thr Arg Glu  
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Ala Gln Asp Glu Phe Ala Val Gly Ser Gln Asn Lys Ala Glu Ala Ala  
260 265 270

Gln Lys Ala Gly Lys Phe Asp Glu Glu Ile Val Pro Val Leu Ile Pro  
275 280 285

Gln Arg Lys Gly Asp Pro Val Ala Phe Lys Thr Asp Glu Phe Val Arg  
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Gln Gly Ala Thr Leu Asp Ser Met Ser Gly Leu Lys Pro Ala Phe Asp  
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Lys Ala Gly Thr Val Thr Ala Ala Asn Ala Ser Gly Leu Asn Asp Gly  
325 330 335

Ala Ala Ala Val Val Val Met Ser Ala Ala Lys Ala Lys Glu Leu Gly  
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Leu Thr Pro Leu Ala Thr Ile Lys Ser Tyr Ala Asn Ala Gly Val Asp  
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Pro Lys Val Met Gly Met Gly Pro Val Pro Ala Ser Lys Arg Ala Leu  
370 375 380

Ser Arg Ala Glu Trp Thr Pro Gln Asp Leu Asp Leu Met Glu Ile Asn  
385 390 395 400

Glu Ala Phe Ala Ala Gln Ala Leu Ala Val His Gln Gln Met Gly Trp  
405 410 415

Asp Thr Ser Lys Val Asn Val Asn Gly Gly Ala Ile Ala Ile Gly His  
420 425 430

Pro Ile Gly Ala Ser Gly Cys Arg Ile Leu Val Thr Leu Leu His Glu  
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Gly Gly Met Gly Val Ala Leu Ala Val Glu Arg Lys  
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<211> 1529

<212> DNA

<213> Rastonia Eutropia

<400> 12

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<212> DNA

<213> Rastonia Eutropia

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<221> CDS

<222> (1)..(987)

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Ser Arg Gly Gln Ser Ala Ala Met Ala Pro Phe Gly Gly Leu Lys Ser
20 25 30

atg act gga ttc cca gtg aag aag gtc aac act gac att act tcc att 144
Met Thr Gly Phe Pro Val Lys Lys Val Asn Thr Asp Ile Thr Ser Ile
35 40 45

aca agc aat ggt gga aga gta aag tgc atg cag gtg tgg cct cca att 192
Thr Ser Asn Gly Gly Arg Val Lys Cys Met Gln Val Trp Pro Pro Ile
50 55 60

gga aag aag aag ttt gag act ctt tcc tat ttg cca cca ttg acc aga 240
Gly Lys Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg
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ggg atc gga acc gcc att tgc cag cgg ctg gcc aag gat ggc ttt cgt Gly Ile Gly Thr Ala Ile Cys Gln Arg Leu Ala Lys Asp Gly Phe Arg 100 105 110	336
gtg gtg gcc ggt tgc ggc ccc aac tcg ccg cgc cgc gaa aag tgg ctg Val Val Ala Gly Cys Gly Pro Asn Ser Pro Arg Arg Glu Lys Trp Leu 115 120 125	384
gag cag cag aag gca ctg ggc ttc gat ttc att gcc tcg gaa ggc aat Glu Gln Gln Lys Ala Leu Gly Phe Asp Phe Ile Ala Ser Glu Gly Asn 130 135 140	432
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atg gtc aag gcg atc cgc cag gac gtg ctc gac aag atc gtc gcg acg Met Val Lys Ala Ile Arg Gln Asp Val Leu Asp Lys Ile Val Ala Thr 275 280 285	864
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Ile Pro Val Lys Arg Leu Gly Leu Pro Glu Glu Ile Ala Ser Ile Cys  
 290 295 300

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 Ala Trp Leu Ser Ser Glu Glu Ser Gly Phe Ser Thr Gly Ala Asp Phe  
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<211> 329

<212> PRT

<213> Rastonia Eutropia

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 35 40 45

Thr Ser Asn Gly Gly Arg Val Lys Cys Met Gln Val Trp Pro Pro Ile  
 50 55 60

Gly Lys Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg  
 65 70 75 80

Asp Ser Arg Val Thr Gln Arg Ile Ala Tyr Val Thr Gly Gly Met Gly  
 85 90 95

Gly Ile Gly Thr Ala Ile Cys Gln Arg Leu Ala Lys Asp Gly Phe Arg  
 100 105 110

Val Val Ala Gly Cys Gly Pro Asn Ser Pro Arg Arg Glu Lys Trp Leu  
 115 120 125

Glu Gln Gln Lys Ala Leu Gly Phe Asp Phe Ile Ala Ser Glu Gly Asn  
 130 135 140

Val Ala Asp Trp Asp Ser Thr Lys Thr Ala Phe Asp Lys Val Lys Ser  
 145 150 155 160

Glu Val Gly Glu Val Asp Val Leu Ile Asn Asn Ala Gly Ile Thr Arg  
 165 170 175

Asp Val Val Phe Arg Lys Met Thr Arg Ala Asp Trp Asp Ala Val Ile  
 180 185 190

Asp Thr Asn Leu Thr Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp  
 195 200 205

Gly Met Ala Asp Arg Gly Trp Gly Arg Ile Val Asn Ile Ser Ser Val  
 210 215 220

Asn Gly Gln Lys Gly Gln Phe Gly Gln Thr Asn Tyr Ser Thr Ala Lys  
 225 230 235 240

Ala Gly Leu His Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Thr  
 245 250 255

Lys Gly Val Thr Val Asn Thr Val Ser Pro Gly Tyr Ile Ala Thr Asp  
 260 265 270

Met Val Lys Ala Ile Arg Gln Asp Val Leu Asp Lys Ile Val Ala Thr  
 275 280 285

Ile Pro Val Lys Arg Leu Gly Leu Pro Glu Glu Ile Ala Ser Ile Cys  
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Ser Leu Asn Gly Gly Leu His Met Gly  
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<211> 1032

<212> DNA

<213> Rastonia Eutropia

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aagaaggtca aactgacat tacttccatt acaagcaatg gtggaagagt aaagtgcattg      180
caggtgtggc ctccaattgg aaagaagaag tttagactc tttcctatth gccaccattg      240
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gtgttccgca agatgacccg cgccgactgg gatgcggtga tcgacaccaa cctgacctcg      600
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caggacgtgc tcgacaagat cgtcgcgacg atcccgggtca agcgccctggg cctgccagaa      900
gagatcgctc cgatctgcgc ctggttgctg tcggaggagt ccggtttctc gaccggcgcc      960
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Ser	Arg	Gly	Gln	Ser	Ala	Ala	Met	Ala	Pro	Phe	Gly	Gly	Leu	Lys	Ser	
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Thr	Ser	Asn	Gly	Gly	Arg	Val	Lys	Cys	Met	Gln	Val	Trp	Pro	Pro	Ile	
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Gly	Lys	Lys	Lys	Phe	Glu	Thr	Leu	Ser	Tyr	Leu	Pro	Pro	Leu	Thr	Arg	
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gat	tcc	cgg	gtg	gcg	acc	ggc	aaa	ggc	gcg	gca	gct	tcc	acg	cag	gaa	288
Asp	Ser	Arg	Val	Ala	Thr	Gly	Lys	Gly	Ala	Ala	Ala	Ser	Thr	Gln	Glu	
				85					90					95		

ggc	aag	tcc	caa	cca	ttc	aag	gtc	acg	ccg	ggg	cca	ttc	gat	cca	gcc	336
Gly	Lys	Ser	Gln	Pro	Phe	Lys	Val	Thr	Pro	Gly	Pro	Phe	Asp	Pro	Ala	
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aca	tgg	ctg	gaa	tgg	tcc	cgc	cag	tgg	cag	ggc	act	gaa	ggc	aac	ggc	384
Thr	Trp	Leu	Glu	Trp	Ser	Arg	Gln	Trp	Gln	Gly	Thr	Glu	Gly	Asn	Gly	
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cac	gcg	gcc	gcg	tcc	ggc	att	ccg	ggc	ctg	gat	gcg	ctg	gca	ggc	gtc	432
His	Ala	Ala	Ala	Ser	Gly	Ile	Pro	Gly	Leu	Asp	Ala	Leu	Ala	Gly	Val	
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Lys	Ile	Ala	Pro	Ala	Gln	Leu	Gly	Asp	Ile	Gln	Gln	Arg	Tyr	Met	Lys	
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gac	ttc	tca	gcg	ctg	tgg	cag	gcc	atg	gcc	gag	ggc	aag	gcc	gag	gcc	528
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Asp	Phe	Ser	Ala	Leu	Trp	Gln	Ala	Met	Ala	Glu	Gly	Lys	Ala	Glu	Ala	
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Thr	Gly	Pro	Leu	His	Asp	Arg	Arg	Phe	Ala	Gly	Asp	Ala	Trp	Arg	Thr	
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Asn	Leu	Pro	Tyr	Arg	Phe	Ala	Ala	Ala	Phe	Tyr	Leu	Leu	Asn	Ala	Arg	
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Gln	Arg	Ile	Arg	Phe	Ala	Ile	Ser	Gln	Trp	Val	Asp	Ala	Met	Ser	Pro	
225					230					235					240	
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Ser	Gly	Gly	Glu	Ser	Leu	Arg	Ala	Gly	Val	Arg	Asn	Met	Met	Glu	Asp	
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Leu	Thr	Arg	Gly	Lys	Ile	Ser	Gln	Thr	Asp	Glu	Ser	Ala	Phe	Glu	Val	
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ggc	cgc	aat	gtc	gcg	gtg	acc	gaa	ggc	gcc	gtg	gtc	ttc	gag	aac	gag	912
Gly	Arg	Asn	Val	Ala	Val	Thr	Glu	Gly	Ala	Val	Val	Phe	Glu	Asn	Glu	
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tac	ttc	cag	ctg	ttg	cag	tac	aag	ccg	ctg	acc	gac	aag	gtg	cac	gcg	960
Tyr	Phe	Gln	Leu	Leu	Gln	Tyr	Lys	Pro	Leu	Thr	Asp	Lys	Val	His	Ala	
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cgc	ccg	ctg	ctg	atg	gtg	ccg	ccg	tgc	atc	aac	aag	tac	tac	atc	ctg	1008
Arg	Pro	Leu	Leu	Met	Val	Pro	Pro	Cys	Ile	Asn	Lys	Tyr	Tyr	Ile	Leu	
				325					330					335		
gac	ctg	cag	ccg	gag	agc	tcg	ctg	gtg	cgc	cat	gtg	gtg	gag	cag	gga	1056
Asp	Leu	Gln	Pro	Glu	Ser	Ser	Leu	Val	Arg	His	Val	Val	Glu	Gln	Gly	
			340					345					350			
cat	acg	gtg	ttt	ctg	gtg	tcg	tgg	cgc	aat	ccg	gac	gcc	agc	atg	gcc	1104
His	Thr	Val	Phe	Leu	Val	Ser	Trp	Arg	Asn	Pro	Asp	Ala	Ser	Met	Ala	
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ggc	agc	acc	tgg	gac	gac	tac	atc	gag	cac	gcg	gcc	atc	cgc	gcc	atc	1152
Gly	Ser	Thr	Trp	Asp	Asp	Tyr	Ile	Glu	His	Ala	Ala	Ile	Arg	Ala	Ile	
	370					375					380					

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ctg gac ttt gcc gac acg ggc atc ctc gac gtc ttt gtc gac gag ggc Leu Asp Phe Ala Asp Thr Gly Ile Leu Asp Val Phe Val Asp Glu Gly 435 440 445	1344
cat gtg cag ttg cgc gag gcc acg ctg ggc ggc ggc gcc ggc gcg ccg His Val Gln Leu Arg Glu Ala Thr Leu Gly Gly Gly Ala Gly Ala Pro 450 455 460	1392
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cgc ccg aac gac ctg gtg tgg aac tac gtg gtc gac aac tac ctg aag Arg Pro Asn Asp Leu Val Trp Asn Tyr Val Val Asp Asn Tyr Leu Lys 485 490 495	1488
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acc aac ctg ccg ggg ccg tgg tac tgc tgg tac ctg cgc cac acc tac Thr Asn Leu Pro Gly Pro Trp Tyr Cys Trp Tyr Leu Arg His Thr Tyr 515 520 525	1584
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gcc ggt gtg atc aac ccg ccg gcc aag aac aag cgc agc cac tgg act	1824

Ala Gly Val Ile Asn Pro Pro Ala Lys Asn Lys Arg Ser His Trp Thr	
595 600 605	
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Asn Asp Ala Leu Pro Glu Ser Pro Gln Gln Trp Leu Ala Gly Ala Ile	
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Glu His His Gly Ser Trp Trp Pro Asp Trp Thr Ala Trp Leu Ala Gly	
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Gln Ala Gly Ala Lys Arg Ala Ala Pro Ala Asn Tyr Gly Asn Ala Arg	
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Thr Trp Leu Glu Trp Ser Arg Gln Trp Gln Gly Thr Glu Gly Asn Gly  
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His Ala Ala Ala Ser Gly Ile Pro Gly Leu Asp Ala Leu Ala Gly Val  
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Lys Ile Ala Pro Ala Gln Leu Gly Asp Ile Gln Gln Arg Tyr Met Lys  
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Asp Phe Ser Ala Leu Trp Gln Ala Met Ala Glu Gly Lys Ala Glu Ala  
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Thr Gly Pro Leu His Asp Arg Arg Phe Ala Gly Asp Ala Trp Arg Thr  
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Asn Leu Pro Tyr Arg Phe Ala Ala Ala Phe Tyr Leu Leu Asn Ala Arg  
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Ser Gly Gly Glu Ser Leu Arg Ala Gly Val Arg Asn Met Met Glu Asp  
 260 265 270

Leu Thr Arg Gly Lys Ile Ser Gln Thr Asp Glu Ser Ala Phe Glu Val  
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Gly Arg Asn Val Ala Val Thr Glu Gly Ala Val Val Phe Glu Asn Glu  
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Tyr Phe Gln Leu Leu Gln Tyr Lys Pro Leu Thr Asp Lys Val His Ala  
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Arg Pro Leu Leu Met Val Pro Pro Cys Ile Asn Lys Tyr Tyr Ile Leu  
325 330 335

Asp Leu Gln Pro Glu Ser Ser Leu Val Arg His Val Val Glu Gln Gly  
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His Thr Val Phe Leu Val Ser Trp Arg Asn Pro Asp Ala Ser Met Ala  
355 360 365

Gly Ser Thr Trp Asp Asp Tyr Ile Glu His Ala Ala Ile Arg Ala Ile  
370 375 380

Glu Val Ala Arg Asp Ile Ser Gly Gln Asp Lys Ile Asn Val Leu Gly  
385 390 395 400

Phe Cys Val Gly Gly Thr Ile Val Ser Thr Ala Leu Ala Val Leu Ala  
405 410 415

Ala Arg Gly Glu His Pro Ala Ala Ser Val Thr Leu Leu Thr Thr Leu  
420 425 430

Leu Asp Phe Ala Asp Thr Gly Ile Leu Asp Val Phe Val Asp Glu Gly  
435 440 445

His Val Gln Leu Arg Glu Ala Thr Leu Gly Gly Gly Ala Gly Ala Pro  
450 455 460

Cys Ala Leu Leu Arg Gly Leu Glu Leu Ala Asn Thr Phe Ser Phe Leu  
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Arg Pro Asn Asp Leu Val Trp Asn Tyr Val Val Asp Asn Tyr Leu Lys  
485 490 495

Gly Asn Thr Pro Val Pro Phe Asp Leu Leu Phe Trp Asn Gly Asp Ala  
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Thr Asn Leu Pro Gly Pro Trp Tyr Cys Trp Tyr Leu Arg His Thr Tyr  
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Leu Gln Asn Glu Leu Lys Val Pro Gly Lys Leu Thr Val Cys Gly Val  
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Pro Val Asp Leu Ala Ser Ile Asp Val Pro Thr Tyr Ile Tyr Gly Ser  
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Arg Glu Asp His Ile Val Pro Trp Thr Ala Ala Tyr Ala Ser Thr Ala  
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Leu Leu Ala Asn Lys Leu Arg Phe Val Leu Gly Ala Ser Gly His Ile  
 580 585 590

Ala Gly Val Ile Asn Pro Pro Ala Lys Asn Lys Arg Ser His Trp Thr  
 595 600 605

Asn Asp Ala Leu Pro Glu Ser Pro Gln Gln Trp Leu Ala Gly Ala Ile  
 610 615 620

Glu His His Gly Ser Trp Trp Pro Asp Trp Thr Ala Trp Leu Ala Gly  
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aagaaggtca aactgacat tacttccatt acaagcaatg gtggaagagt aaagtgcattg 180

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<212> DNA

<213> *P. aeruginosa*

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Thr Leu Asn Leu Asn Pro Val Ile Gly Ile Arg Gly Lys Asp Leu Leu
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acc tcc gcg cgc atg gtc ctg ctc cag gcg gtg cgc cag ccg ctg cac 144
Thr Ser Ala Arg Met Val Leu Leu Gln Ala Val Arg Gln Pro Leu His
35 40 45

agc gcc agg cac gtg gcg cat ttc agc ctg gag ctg aag aac gtc ctg 192
Ser Ala Arg His Val Ala His Phe Ser Leu Glu Leu Lys Asn Val Leu
50 55 60

ctc ggc cag tcg gag cta cgc cca ggc gat gac gac cga cgc ttt tcc 240
Leu Gly Gln Ser Glu Leu Arg Pro Gly Asp Asp Asp Arg Arg Phe Ser
65 70 75 80

gat ccg gcc tgg agc cag aat cca ctg tac aag cgc tac atg cag acc 288
Asp Pro Ala Trp Ser Gln Asn Pro Leu Tyr Lys Arg Tyr Met Gln Thr
85 90 95

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Leu Ser Pro Gln Asp Ile Ser Arg Gly Gln Phe Val Ile Asn Leu Leu	
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acc gag gcg atg tcg ccg acc aac agc ctg agc aac ccg gcg gcg gtc	432
Thr Glu Ala Met Ser Pro Thr Asn Ser Leu Ser Asn Pro Ala Ala Val	
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Lys Arg Phe Phe Glu Thr Gly Gly Lys Ser Leu Leu Asp Gly Leu Gly	
145 150 155 160	
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His Leu Ala Lys Asp Leu Val Asn Asn Gly Gly Met Pro Ser Gln Val	
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Asp Met Asp Ala Phe Glu Val Gly Lys Asn Leu Ala Thr Thr Glu Gly	
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Ala Val Val Phe Arg Asn Asp Val Leu Glu Leu Ile Gln Tyr Arg Pro	
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Ile Thr Glu Ser Val His Glu Arg Pro Leu Leu Val Val Pro Pro Gln	
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Arg Phe Cys Leu Arg Asn Gly Val Gln Thr Phe Ile Val Ser Trp Arg	
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Asn Pro Thr Lys Ser Gln Arg Glu Trp Gly Leu Thr Thr Tyr Ile Glu	
260 265 270	
gcg ctc aag gag gcc atc gag gta gtc ctg tcg atc acc ggc agc aag	864
Ala Leu Lys Glu Ala Ile Glu Val Val Leu Ser Ile Thr Gly Ser Lys	
275 280 285	
gac ctc aac ctc ctc ggc gcc tgc tcc ggc ggg atc acc acc gcg acc	912
Asp Leu Asn Leu Leu Gly Ala Cys Ser Gly Gly Ile Thr Thr Ala Thr	
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ctg gtc ggc cac tac gtg gcc agc ggc gag aag aag gtc aac gcc ttc	960

Leu	Val	Gly	His	Tyr	Val	Ala	Ser	Gly	Glu	Lys	Lys	Val	Asn	Ala	Phe	
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Thr	Gln	Leu	Val	Ser	Val	Leu	Asp	Phe	Glu	Leu	Asn	Thr	Gln	Val	Ala	
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Leu	Phe	Ala	Asp	Glu	Lys	Thr	Leu	Glu	Ala	Ala	Lys	Arg	Arg	Ser	Tyr	
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Gln	Ser	Gly	Val	Leu	Glu	Gly	Lys	Asp	Met	Ala	Lys	Val	Phe	Ala	Trp	
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Met	Arg	Pro	Asn	Asp	Leu	Ile	Trp	Asn	Tyr	Trp	Val	Asn	Asn	Tyr	Leu	
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Lys	Ser	Asn	Pro	Leu	Asn	Arg	Pro	Gly	Ala	Leu	Glu	Val	Ser	Gly	Thr	
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Pro	Ile	Asp	Leu	Lys	Gln	Val	Thr	Cys	Asp	Phe	Tyr	Cys	Val	Ala	Gly	
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cag	agc	atc	ctc	aac	cca	ccg	ggc	aac	ccc	aag	gca	cgc	ttc	atg	acc	1488
Gln	Ser	Ile	Leu	Asn	Pro	Pro	Gly	Asn	Pro	Lys	Ala	Arg	Phe	Met	Thr	
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aat	ccg	gaa	ctg	ccc	gcc	gag	ccc	aag	gcc	tgg	ctg	gaa	cag	gcc	ggc	1536
Asn	Pro	Glu	Leu	Pro	Ala	Glu	Pro	Lys	Ala	Trp	Leu	Glu	Gln	Ala	Gly	
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Lys	His	Ala	Asp	Ser	Trp	Trp	Leu	His	Trp	Gln	Gln	Trp	Leu	Ala	Glu	
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<213> P. aeruginosa

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Thr Ser Ala Arg Met Val Leu Leu Gln Ala Val Arg Gln Pro Leu His  
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Ser Ala Arg His Val Ala His Phe Ser Leu Glu Leu Lys Asn Val Leu  
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Leu Gly Gln Ser Glu Leu Arg Pro Gly Asp Asp Asp Arg Arg Phe Ser  
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Asp Pro Ala Trp Ser Gln Asn Pro Leu Tyr Lys Arg Tyr Met Gln Thr  
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Tyr Leu Ala Trp Arg Lys Glu Leu His Ser Trp Ile Ser His Ser Asp  
100 105 110

Leu Ser Pro Gln Asp Ile Ser Arg Gly Gln Phe Val Ile Asn Leu Leu  
115 120 125



Thr Glu Ala Met Ser Pro Thr Asn Ser Leu Ser Asn Pro Ala Ala Val  
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Lys Arg Phe Phe Glu Thr Gly Gly Lys Ser Leu Leu Asp Gly Leu Gly  
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His Leu Ala Lys Asp Leu Val Asn Asn Gly Gly Met Pro Ser Gln Val  
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Ala Val Val Phe Arg Asn Asp Val Leu Glu Leu Ile Gln Tyr Arg Pro  
 195 200 205

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Ile Asn Lys Phe Tyr Val Phe Asp Leu Ser Pro Asp Lys Ser Leu Ala  
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Thr Thr Arg Leu Pro Ala Ala Leu His Gly Glu Phe Val Glu Leu Phe  
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Lys Ser Asn Pro Leu Asn Arg Pro Gly Ala Leu Glu Val Ser Gly Thr  
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Pro Ile Asp Leu Lys Gln Val Thr Cys Asp Phe Tyr Cys Val Ala Gly  
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Leu Asn Asp His Ile Thr Pro Trp Glu Ser Cys Tyr Lys Ser Ala Arg  
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Leu Leu Gly Gly Lys Cys Glu Phe Ile Leu Ser Asn Ser Gly His Ile  
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Gln Ser Ile Leu Asn Pro Pro Gly Asn Pro Lys Ala Arg Phe Met Thr  
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Lys His Ala Asp Ser Trp Trp Leu His Trp Gln Gln Trp Leu Ala Glu  
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&lt;211&gt; 1692

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<213> *P. aeruginosa*

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Ser Ala Arg His Val Ala His Phe Ser Leu Glu Leu Lys Asn Val Leu
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Leu Gly Gln Ser Glu Leu Arg Pro Gly Asp Asp Arg Arg Phe Ser
65 70 75 80

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Tyr Leu Ala Trp Arg Lys Glu Leu His Ser Trp Ile Ser His Ser Asp	
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Thr Glu Ala Met Ser Pro Thr Asn Ser Leu Ser Asn Pro Ala Ala Val	
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Lys Arg Phe Phe Glu Thr Gly Gly Lys Ser Leu Leu Asp Gly Leu Gly	
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Asn Pro Thr Lys Ser Gln Arg Glu Trp Gly Leu Thr Thr Tyr Ile Glu	
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Lys	Ser	Asn	Pro	Leu	Asn	Arg	Pro	Gly	Ala	Leu	Glu	Val	Ser	Gly	Thr	
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Pro	Ile	Asp	Leu	Lys	Gln	Val	Thr	Cys	Asp	Phe	Tyr	Cys	Val	Ala	Gly	
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ctg	aac	gac	cac	atc	acc	ccc	tgg	gag	tcg	tgc	tac	aag	tcg	gcc	agg	1392
Leu	Asn	Asp	His	Ile	Thr	Pro	Trp	Glu	Ser	Cys	Tyr	Lys	Ser	Ala	Arg	
	450					455					460					
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Leu	Leu	Gly	Gly	Lys	Cys	Glu	Phe	Ile	Leu	Ser	Asn	Ser	Gly	His	Ile	
465					470					475					480	
cag	agc	atc	ctc	aac	cca	ccg	ggc	aac	ccc	aag	gca	cgc	ttc	atg	acc	1488
Gln	Ser	Ile	Leu	Asn	Pro	Pro	Gly	Asn	Pro	Lys	Ala	Arg	Phe	Met	Thr	
				485					490					495		
aat	ccg	gaa	ctg	ccc	gcc	gag	ccc	aag	gcc	tgg	ctg	gaa	cag	gcc	ggc	1536
Asn	Pro	Glu	Leu	Pro	Ala	Glu	Pro	Lys	Ala	Trp	Leu	Glu	Gln	Ala	Gly	
			500					505					510			

aag cac gcc gac tcg tgg tgg ttg cac tgg cag caa tgg ctg gcc gaa 1584  
Lys His Ala Asp Ser Trp Trp Leu His Trp Gln Gln Trp Leu Ala Glu  
515 520 525

cgc tcc ggc aag acc cgc aag gcg ccc gcc agc ctg ggc aac aag acc 1632  
 Arg Ser Gly Lys Thr Arg Lys Ala Pro Ala Ser Leu Gly Asn Lys Thr  
 530 535 540

tat	ccg	gcc	ggc	gaa	gcc	gcg	ccc	gga	acc	tac	gtg	cat	gaa	cga	tca	1680
Tyr	Pro	Ala	Gly	Glu	Ala	Ala	Pro	Gly	Thr	Tyr	Val	His	Glu	Arg	Ser	
545					550					555					560	

aaa gct ttg ggc aaa ggt gtt acc gag gaa caa ttc aaa gag acc tgg 1728  
Lys Ala Leu Gly Lys Gly Val Thr Glu Glu Gln Phe Lys Glu Thr Trp  
565 570 575

acg agg ccg gga gct gct gga atg ggc gaa ggg act agc ctt gtg gtg 1776  
Thr Arg Pro Gly Ala Ala Gly Met Gly Glu Gly Thr Ser Leu Val Val  
580 585 590

gcc aag tcc aga atg taa 1794  
Ala Lys Ser Arg Met  
595

<210> 23

<211> 597

<212> PRT

<213> P. aeruginosa

<400> 23

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20 25 30

Thr Ser Ala Arg Met Val Leu Leu Gln Ala Val Arg Gln Pro Leu His  
35 40 45

Ser Ala Arg His Val Ala His Phe Ser Leu Glu Leu Lys Asn Val Leu  
50 55 60

Leu Gly Gln Ser Glu Leu Arg Pro Gly Asp Asp Asp Arg Arg Phe Ser  
65 70 75 80

Asp Pro Ala Trp Ser Gln Asn Pro Leu Tyr Lys Arg Tyr Met Gln Thr  
85 90 95

Tyr Leu Ala Trp Arg Lys Glu Leu His Ser Trp Ile Ser His Ser Asp  
100 105 110

Leu Ser Pro Gln Asp Ile Ser Arg Gly Gln Phe Val Ile Asn Leu Leu  
115 120 125

Thr Glu Ala Met Ser Pro Thr Asn Ser Leu Ser Asn Pro Ala Ala Val  
130 135 140

Lys Arg Phe Phe Glu Thr Gly Gly Lys Ser Leu Leu Asp Gly Leu Gly  
145 150 155 160

His Leu Ala Lys Asp Leu Val Asn Asn Gly Gly Met Pro Ser Gln Val  
165 170 175

Asp Met Asp Ala Phe Glu Val Gly Lys Asn Leu Ala Thr Thr Glu Gly  
180 185 190

Ala Val Val Phe Arg Asn Asp Val Leu Glu Leu Ile Gln Tyr Arg Pro  
195 200 205

Ile Thr Glu Ser Val His Glu Arg Pro Leu Leu Val Val Pro Pro Gln  
210 215 220

Ile Asn Lys Phe Tyr Val Phe Asp Leu Ser Pro Asp Lys Ser Leu Ala  
225 230 235 240

Arg Phe Cys Leu Arg Asn Gly Val Gln Thr Phe Ile Val Ser Trp Arg  
245 250 255

Asn Pro Thr Lys Ser Gln Arg Glu Trp Gly Leu Thr Thr Tyr Ile Glu  
260 265 270

Ala Leu Lys Glu Ala Ile Glu Val Val Leu Ser Ile Thr Gly Ser Lys  
275 280 285



Asp Leu Asn Leu Leu Gly Ala Cys Ser Gly Gly Ile Thr Thr Ala Thr  
 290 295 300

Leu Val Gly His Tyr Val Ala Ser Gly Glu Lys Lys Val Asn Ala Phe  
 305 310 315 320

Thr Gln Leu Val Ser Val Leu Asp Phe Glu Leu Asn Thr Gln Val Ala  
 325 330 335

Leu Phe Ala Asp Glu Lys Thr Leu Glu Ala Ala Lys Arg Arg Ser Tyr  
 340 345 350

Gln Ser Gly Val Leu Glu Gly Lys Asp Met Ala Lys Val Phe Ala Trp  
 355 360 365

Met Arg Pro Asn Asp Leu Ile Trp Asn Tyr Trp Val Asn Asn Tyr Leu  
 370 375 380

Leu Gly Asn Gln Pro Pro Ala Phe Asp Ile Leu Tyr Trp Asn Asn Asp  
 385 390 395 400

Thr Thr Arg Leu Pro Ala Ala Leu His Gly Glu Phe Val Glu Leu Phe  
 405 410 415

Lys Ser Asn Pro Leu Asn Arg Pro Gly Ala Leu Glu Val Ser Gly Thr  
 420 425 430

Pro Ile Asp Leu Lys Gln Val Thr Cys Asp Phe Tyr Cys Val Ala Gly  
 435 440 445

Leu Asn Asp His Ile Thr Pro Trp Glu Ser Cys Tyr Lys Ser Ala Arg  
 450 455 460

Leu Leu Gly Gly Lys Cys Glu Phe Ile Leu Ser Asn Ser Gly His Ile  
 465 470 475 480

Gln Ser Ile Leu Asn Pro Pro Gly Asn Pro Lys Ala Arg Phe Met Thr  
 485 490 495

Asn Pro Glu Leu Pro Ala Glu Pro Lys Ala Trp Leu Glu Gln Ala Gly  
                   500                  505                  510

Lys His Ala Asp Ser Trp Trp Leu His Trp Gln Gln Trp Leu Ala Glu  
           515                  520                  525

Arg Ser Gly Lys Thr Arg Lys Ala Pro Ala Ser Leu Gly Asn Lys Thr  
       530                  535                  540

Tyr Pro Ala Gly Glu Ala Ala Pro Gly Thr Tyr Val His Glu Arg Ser  
       545                  550                  555                  560

Lys Ala Leu Gly Lys Gly Val Thr Glu Glu Gln Phe Lys Glu Thr Trp  
                   565                  570                  575

Thr Arg Pro Gly Ala Ala Gly Met Gly Glu Gly Thr Ser Leu Val Val  
           580                  585                  590

Ala Lys Ser Arg Met  
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<210> 24

<211> 1883

<212> DNA

<213> P. aeruginosa

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 gcgcattggtc ctgctccagg cggatgcgcca gccgctgcac agcgccaggc acgtggcgca 180  
 tttcagcctg gagctgaaga acgtcctgct cggccagtcg gagctacgcc caggcgatga 240  
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 caacagcctg agcaacccgg cggcgggtcaa gcgcttcttc gagaccggcg gcaagagcct 480

gctggacggc ctcggccacc tggccaagga cctggtgaac aacggcgga tgccgagcca 540  
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 gttccgcaac gacgtgctgg aactgatcca gtaccggccg atcaccgagt cgggtgcacga 660  
 acgcccgtg ctggtggtgc cgccgcagat caacaagttc tacgtcttcg acctgtcgcc 720  
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 gcgcaacccg accaagtcgc agcggaatg gggcctgacc acctatatcg aggcgctcaa 840  
 ggaggccatc gaggtagtcc tgtcgatcac cggcagcaag gacctcaacc tcctcggcgc 900  
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 gaaggtcaac gccttcaccc aactggtcag cgtgctcgac ttcgaactga ataccaggt 1020  
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 caacagcggc cacatccaga gcatcctcaa cccaccgggc aacccaagg cacgcttcat 1500  
 gaccaatccg gaactgccc cgcagccaa ggctggctg gaacaggccg gcaagcacgc 1560  
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<210> 25

<211> 1929

&lt;212&gt; DNA

&lt;213&gt; P. aeruginosa

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1929)

&lt;400&gt; 25

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Met	Ala	Ser	Met	Ile	Ser	Ser	Ser	Ala	Val	Thr	Thr	Val	Ser	Arg	Ala	
1				5					10					15		

tct	agg	ggg	caa	tcc	gcc	gca	atg	gct	cca	ttc	ggc	ggc	ctc	aaa	tcc	96
Ser	Arg	Gly	Gln	Ser	Ala	Ala	Met	Ala	Pro	Phe	Gly	Gly	Leu	Lys	Ser	
			20					25					30			

atg	act	gga	ttc	cca	gtg	aag	aag	gtc	aac	act	gac	att	act	tcc	att	144
Met	Thr	Gly	Phe	Pro	Val	Lys	Lys	Val	Asn	Thr	Asp	Ile	Thr	Ser	Ile	
		35					40					45				

aca	agc	aat	ggt	gga	aga	gta	aag	tgc	atg	cag	gtg	tgg	cct	cca	att	192
Thr	Ser	Asn	Gly	Gly	Arg	Val	Lys	Cys	Met	Gln	Val	Trp	Pro	Pro	Ile	
		50				55					60					

gga	aag	aag	aag	ttt	gag	act	ctt	tcc	tat	ttg	cca	cca	ttg	acc	aga	240
Gly	Lys	Lys	Lys	Phe	Glu	Thr	Leu	Ser	Tyr	Leu	Pro	Pro	Leu	Thr	Arg	
65					70					75					80	

gat	tcc	cgg	gtg	agt	cag	aag	aac	aat	aac	gag	ctt	ccc	aag	caa	gcc	288
Asp	Ser	Arg	Val	Ser	Gln	Lys	Asn	Asn	Asn	Glu	Leu	Pro	Lys	Gln	Ala	
				85					90					95		

gcg	gaa	aac	acg	ctg	aac	ctg	aat	ccg	gtg	atc	ggc	atc	cgg	ggc	aag	336
Ala	Glu	Asn	Thr	Leu	Asn	Leu	Asn	Pro	Val	Ile	Gly	Ile	Arg	Gly	Lys	
			100					105						110		

gac	ctg	ctc	acc	tcc	gcg	cgc	atg	gtc	ctg	ctc	cag	gcg	gtg	cgc	cag	384
Asp	Leu	Leu	Thr	Ser	Ala	Arg	Met	Val	Leu	Leu	Gln	Ala	Val	Arg	Gln	
			115				120					125				

ccg	ctg	cac	agc	gcc	agg	cac	gtg	gcg	cat	ttc	agc	ctg	gag	ctg	aag	432
Pro	Leu	His	Ser	Ala	Arg	His	Val	Ala	His	Phe	Ser	Leu	Glu	Leu	Lys	
			130			135					140					

aac	gtc	ctg	ctc	ggc	cag	tcg	gag	cta	cgc	cca	ggc	gat	gac	gac	cga	480
Asn	Val	Leu	Leu	Gly	Gln	Ser	Glu	Leu	Arg	Pro	Gly	Asp	Asp	Asp	Arg	
145					150					155					160	

cgc ttt tcc gat ccg gcc tgg agc cag aat cca ctg tac aag cgc tac	528
Arg Phe Ser Asp Pro Ala Trp Ser Gln Asn Pro Leu Tyr Lys Arg Tyr	
165 170 175	
atg cag acc tac ctg gcc tgg cgc aag gag ctg cac agc tgg atc agc	576
Met Gln Thr Tyr Leu Ala Trp Arg Lys Glu Leu His Ser Trp Ile Ser	
180 185 190	
cac agc gac ctg tcg ccg cag gac atc agt cgt ggc cag ttc gtc atc	624
His Ser Asp Leu Ser Pro Gln Asp Ile Ser Arg Gly Gln Phe Val Ile	
195 200 205	
aac ctg ctg acc gag gcg atg tcg ccg acc aac agc ctg agc aac ccg	672
Asn Leu Leu Thr Glu Ala Met Ser Pro Thr Asn Ser Leu Ser Asn Pro	
210 215 220	
gcg gcg gtc aag cgc ttc ttc gag acc ggc ggc aag agc ctg ctg gac	720
Ala Ala Val Lys Arg Phe Phe Glu Thr Gly Gly Lys Ser Leu Leu Asp	
225 230 235 240	
ggc ctc ggc cac ctg gcc aag gac ctg gtg aac aac ggc ggg atg ccg	768
Gly Leu Gly His Leu Ala Lys Asp Leu Val Asn Asn Gly Gly Met Pro	
245 250 255	
agc cag gtg gac atg gac gcc ttc gag gtg ggc aag aac ctg gcc acc	816
Ser Gln Val Asp Met Asp Ala Phe Glu Val Gly Lys Asn Leu Ala Thr	
260 265 270	
acc gag ggc gcc gtg gtg ttc cgc aac gac gtg ctg gaa ctg atc cag	864
Thr Glu Gly Ala Val Val Phe Arg Asn Asp Val Leu Glu Leu Ile Gln	
275 280 285	
tac cgg ccg atc acc gag tcg gtg cac gaa cgc ccg ctg ctg gtg gtg	912
Tyr Arg Pro Ile Thr Glu Ser Val His Glu Arg Pro Leu Leu Val Val	
290 295 300	
ccg ccg cag atc aac aag ttc tac gtc ttc gac ctg tcg ccg gac aag	960
Pro Pro Gln Ile Asn Lys Phe Tyr Val Phe Asp Leu Ser Pro Asp Lys	
305 310 315 320	
agc ctg gcg cgc ttc tgc ctg cgc aac ggc gtg cag acc ttc atc gtc	1008
Ser Leu Ala Arg Phe Cys Leu Arg Asn Gly Val Gln Thr Phe Ile Val	
325 330 335	
agt tgg cgc aac ccg acc aag tcg cag cgc gaa tgg ggc ctg acc acc	1056
Ser Trp Arg Asn Pro Thr Lys Ser Gln Arg Glu Trp Gly Leu Thr Thr	
340 345 350	
tat atc gag gcg ctc aag gag gcc atc gag gta gtc ctg tcg atc acc	1104
Tyr Ile Glu Ala Leu Lys Glu Ala Ile Glu Val Val Leu Ser Ile Thr	
355 360 365	
ggc agc aag gac ctc aac ctc ctc ggc gcc tgc tcc ggc ggg atc acc	1152

Gly 370	Ser	Lys	Asp	Leu	Asn 375	Leu	Leu	Gly	Ala	Cys 380	Ser	Gly	Gly	Ile	Thr	
acc	gcg	acc	ctg	gtc	ggc	cac	tac	gtg	gcc	agc	ggc	gag	aag	aag	gtc	1200
Thr 385	Ala	Thr	Leu	Val	Gly 390	His	Tyr	Val	Ala	Ser 395	Gly	Glu	Lys	Lys	Val 400	
aac	gcc	ttc	acc	caa	ctg	gtc	agc	gtg	ctc	gac	ttc	gaa	ctg	aat	acc	1248
Asn	Ala	Phe	Thr	Gln 405	Leu	Val	Ser	Val	Leu 410	Asp	Phe	Glu	Leu	Asn 415	Thr	
cag	gtc	gcg	ctg	ttc	gcc	gac	gag	aag	act	ctg	gag	gcc	gcc	aag	cgt	1296
Gln	Val	Ala	Leu	Phe 420	Ala	Asp	Glu	Lys 425	Thr	Leu	Glu	Ala	Ala 430	Lys	Arg	
cgt	tcc	tac	cag	tcc	ggc	gtg	ctg	gag	ggc	aag	gac	atg	gcc	aag	gtg	1344
Arg	Ser	Tyr	Gln	Ser 435	Gly	Val	Leu 440	Glu	Gly	Lys	Asp	Met 445	Ala	Lys	Val	
ttc	gcc	tgg	atg	cgc	ccc	aac	gac	ctg	atc	tgg	aac	tac	tgg	gtc	aac	1392
Phe 450	Ala	Trp	Met	Arg	Pro 455	Asn	Asp	Leu	Ile	Trp	Asn 460	Tyr	Trp	Val	Asn	
aac	tac	ctg	ctc	ggc	aac	cag	ccg	ccg	gcg	ttc	gac	atc	ctc	tac	tgg	1440
Asn 465	Tyr	Leu	Leu	Gly 470	Asn	Gln	Pro	Pro	Ala	Phe 475	Asp	Ile	Leu	Tyr	Trp 480	
aac	aac	gac	acc	acg	cgc	ctg	ccc	gcc	gcg	ctg	cac	ggc	gag	ttc	gtc	1488
Asn	Asn	Asp	Thr	Thr 485	Arg	Leu	Pro	Ala 490	Ala	Leu	His	Gly	Glu	Phe 495	Val	
gaa	ctg	ttc	aag	agc	aac	ccg	ctg	aac	cgc	ccc	ggc	gcc	ctg	gag	gtc	1536
Glu	Leu	Phe 500	Lys	Ser	Asn	Pro	Leu 505	Asn	Arg	Pro	Gly	Ala 510	Leu	Glu	Val	
tcc	ggc	acg	ccc	atc	gac	ctg	aag	cag	gtg	act	tgc	gac	ttc	tac	tgt	1584
Ser	Gly	Thr 515	Pro	Ile	Asp	Leu 520	Lys	Gln	Val	Thr	Cys 525	Asp	Phe	Tyr	Cys	
gtc	gcc	ggt	ctg	aac	gac	cac	atc	acc	ccc	tgg	gag	tcg	tgc	tac	aag	1632
Val 530	Ala	Gly	Leu	Asn	Asp 535	His	Ile	Thr	Pro	Trp	Glu 540	Ser	Cys	Tyr	Lys	
tcg	gcc	agg	ctg	ctg	ggt	ggc	aag	tgc	gag	ttc	atc	ctc	tcc	aac	agc	1680
Ser 545	Ala	Arg	Leu	Leu 550	Gly	Gly	Lys	Cys	Glu	Phe 555	Ile	Leu	Ser	Asn 560	Ser	
ggt	cac	atc	cag	agc	atc	ctc	aac	cca	ccg	ggc	aac	ccc	aag	gca	cgc	1728
Gly	His	Ile	Gln	Ser 565	Ile	Leu	Asn	Pro	Pro 570	Gly	Asn	Pro	Lys 575	Ala	Arg	
ttc	atg	acc	aat	ccg	gaa	ctg	ccc	gcc	gag	ccc	aag	gcc	tgg	ctg	gaa	1776
Phe	Met	Thr 580	Asn	Pro	Glu	Leu 585	Pro	Ala	Glu	Pro	Lys	Ala 590	Trp	Leu	Glu	

cag gcc ggc aag cac gcc gac tcg tgg tgg ttg cac tgg cag caa tgg 1824  
Gln Ala Gly Lys His Ala Asp Ser Trp Trp Leu His Trp Gln Gln Trp  
595 600 605

ctg gcc gaa cgc tcc ggc aag acc cgc aag gcg ccc gcc agc ctg ggc 1872  
Leu Ala Glu Arg Ser Gly Lys Thr Arg Lys Ala Pro Ala Ser Leu Gly  
610 615 620

aac aag acc tat ccg gcc ggc gaa gcc gcg ccc gga acc tac gtg cat 1920  
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gaa cga tga	1929
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<210> 26

<211> 642

&lt;212&gt; PRT

<213> P. aeruginosa

<400> 26

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Met Thr Gly Phe Pro Val Lys Lys Val Asn Thr Asp Ile Thr Ser Ile  
35 40 45

Thr Ser Asn Gly Gly Arg Val Lys Cys Met Gln Val Trp Pro Pro Ile  
50 55 60

Gly Lys Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg  
65 70 75 80

Asp Ser Arg Val Ser Gln Lys Asn Asn Asn Glu Leu Pro Lys Gln Ala  
85 90 95

Ala Glu Asn Thr Leu Asn Leu Asn Pro Val Ile Gly Ile Arg Gly Lys  
 100 105 110

Asp Leu Leu Thr Ser Ala Arg Met Val Leu Leu Gln Ala Val Arg Gln  
 115 120 125

Pro Leu His Ser Ala Arg His Val Ala His Phe Ser Leu Glu Leu Lys  
 130 135 140

Asn Val Leu Leu Gly Gln Ser Glu Leu Arg Pro Gly Asp Asp Asp Arg  
 145 150 155 160

Arg Phe Ser Asp Pro Ala Trp Ser Gln Asn Pro Leu Tyr Lys Arg Tyr  
 165 170 175

Met Gln Thr Tyr Leu Ala Trp Arg Lys Glu Leu His Ser Trp Ile Ser  
 180 185 190

His Ser Asp Leu Ser Pro Gln Asp Ile Ser Arg Gly Gln Phe Val Ile  
 195 200 205

Asn Leu Leu Thr Glu Ala Met Ser Pro Thr Asn Ser Leu Ser Asn Pro  
 210 215 220

Ala Ala Val Lys Arg Phe Phe Glu Thr Gly Gly Lys Ser Leu Leu Asp  
 225 230 235 240

Gly Leu Gly His Leu Ala Lys Asp Leu Val Asn Asn Gly Gly Met Pro  
 245 250 255

Ser Gln Val Asp Met Asp Ala Phe Glu Val Gly Lys Asn Leu Ala Thr  
 260 265 270

Thr Glu Gly Ala Val Val Phe Arg Asn Asp Val Leu Glu Leu Ile Gln  
 275 280 285

Tyr Arg Pro Ile Thr Glu Ser Val His Glu Arg Pro Leu Leu Val Val  
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Pro Pro Gln Ile Asn Lys Phe Tyr Val Phe Asp Leu Ser Pro Asp Lys  
 305 310 315 320



Ser Leu Ala Arg Phe Cys Leu Arg Asn Gly Val Gln Thr Phe Ile Val  
 325 330 335

Ser Trp Arg Asn Pro Thr Lys Ser Gln Arg Glu Trp Gly Leu Thr Thr  
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Tyr Ile Glu Ala Leu Lys Glu Ala Ile Glu Val Val Leu Ser Ile Thr  
 355 360 365

Gly Ser Lys Asp Leu Asn Leu Leu Gly Ala Cys Ser Gly Gly Ile Thr  
 370 375 380

Thr Ala Thr Leu Val Gly His Tyr Val Ala Ser Gly Glu Lys Lys Val  
 385 390 395 400

Asn Ala Phe Thr Gln Leu Val Ser Val Leu Asp Phe Glu Leu Asn Thr  
 405 410 415

Gln Val Ala Leu Phe Ala Asp Glu Lys Thr Leu Glu Ala Ala Lys Arg  
 420 425 430

Arg Ser Tyr Gln Ser Gly Val Leu Glu Gly Lys Asp Met Ala Lys Val  
 435 440 445

Phe Ala Trp Met Arg Pro Asn Asp Leu Ile Trp Asn Tyr Trp Val Asn  
 450 455 460

Asn Tyr Leu Leu Gly Asn Gln Pro Pro Ala Phe Asp Ile Leu Tyr Trp  
 465 470 475 480

Asn Asn Asp Thr Thr Arg Leu Pro Ala Ala Leu His Gly Glu Phe Val  
 485 490 495

Glu Leu Phe Lys Ser Asn Pro Leu Asn Arg Pro Gly Ala Leu Glu Val  
 500 505 510

Ser Gly Thr Pro Ile Asp Leu Lys Gln Val Thr Cys Asp Phe Tyr Cys  
 515 520 525

Val Ala Gly Leu Asn Asp His Ile Thr Pro Trp Glu Ser Cys Tyr Lys  
 530 535 540

Ser Ala Arg Leu Leu Gly Gly Lys Cys Glu Phe Ile Leu Ser Asn Ser  
 545 550 555 560

Gly His Ile Gln Ser Ile Leu Asn Pro Pro Gly Asn Pro Lys Ala Arg  
 565 570 575

Phe Met Thr Asn Pro Glu Leu Pro Ala Glu Pro Lys Ala Trp Leu Glu  
 580 585 590

Gln Ala Gly Lys His Ala Asp Ser Trp Trp Leu His Trp Gln Gln Trp  
 595 600 605

Leu Ala Glu Arg Ser Gly Lys Thr Arg Lys Ala Pro Ala Ser Leu Gly  
 610 615 620

Asn Lys Thr Tyr Pro Ala Gly Glu Ala Ala Pro Gly Thr Tyr Val His  
 625 630 635 640

Glu Arg

<210> 27

<211> 1941

<212> DNA

<213> *P. aeruginosa*

<400> 27

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aagaaggtca aactgacat tacttccatt acaagcaatg gtggaagagt aaagtgcag	180
caggtgtggc ctccaattgg aaagaagaag tttgagactc tttcctatatt gccaccattg	240
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aacacgctga acctgaatcc ggtgatcggc atccggggca aggacctgct cacctccgcg	360

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gaccgacgct tttccgatcc ggcttgagc cagaatccac tgtacaagcg ctacatgcag	540
acctacctgg cctggcgcaa ggagctgcac agctggatca gccacagcga cctgtcgccg	600
caggacatca gtcgtggcca gttcgtcatc aacctgctga ccgaggcgat gtcgccgacc	660
aacagcctga gcaaccggc ggcggtcaag cgcttcttcg agaccggcg caagagcctg	720
ctggacggcc tcggccacct ggccaaggac ctggtgaaca acggcgggat gccgagccag	780
gtggacatgg acgccttcga ggtgggcaag aacctggcca ccaccgagg cgccgtggtg	840
ttccgcaacg acgtgctgga actgatccag taccggccga tcaccgagtc ggtgcacgaa	900
cgcgcgctgc tgggtggtgcc gccgcagatc aacaagttct acgtcttcga cctgtcgccg	960
gacaagagcc tggcgcgctt ctgcctgcgc aacggcgctgc agaccttcac cgtcagttgg	1020
cgaacccga ccaagtgcga gcgcgaatgg ggcttgacca cctatatcga ggcgctcaag	1080
gaggccatcg aggtagtctt gtcgatcacc ggcagcaagg acctcaacct cctcggcgcc	1140
tgctccggcg ggatcaccac cgcgaccctg gtcggccact acgtggccag cggcgagaag	1200
aaggtaacg ccttcaccca actggtcagc gtgctcgact tcgaactgaa taccaggtc	1260
gcgctgttcg ccgacgagaa gactctggag gccgccaagc gtcgttccta ccagtccggc	1320
gtgctggagg gcaaggacat ggccaagtg ttgcctgga tgcgccccaa cgacctgatc	1380
tggaactact gggtaacaa ctacctgctc ggcaaccagc cgcggcggtt cgacatcctc	1440
tactggaaca acgacaccac gcgcctgcc gccgcgctgc acggcgagtt cgtcgaactg	1500
ttcaagagca acccgctgaa ccgccccggc gccctggagg tctccggcac gcccatcgac	1560
ctgaagcagg tgacttgca cttctactgt gtcgccggtc tgaacgacca catcaccccc	1620
tgggagtcgt gctacaagtc ggccaggctg ctgggtggca agtgcgagtt catcctctcc	1680
aacagcggtc acatccagag catcctcaac ccaccgggca accccaaggc acgcttcatg	1740
accaatccgg aactgcccgc cgagcccaag gcctggctgg aacaggccgg caagcacgcc	1800
gactcgtggt ggttgactg gcagcaatgg ctggccgaac gctccggcaa gacccgcaag	1860
gcgcccgcga gcctgggcaa caagacctat ccggccggcg aagccgcgcc cggaacctac	1920
gtgcatgaac gatgaggtac c	1941

&lt;210&gt; 28

&lt;211&gt; 1137

&lt;212&gt; DNA

<213> *Pseudomonas putida*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1137)

&lt;400&gt; 28

atg gct tct atg ata tcc tct tcc gct gtg aca aca gtc agc cgt gcc	48
Met Ala Ser Met Ile Ser Ser Ser Ala Val Thr Thr Val Ser Arg Ala	
1 5 10 15	

tct agg ggg caa tcc gcc gca atg gct cca ttc ggc ggc ctc aaa tcc	96
Ser Arg Gly Gln Ser Ala Ala Met Ala Pro Phe Gly Gly Leu Lys Ser	
20 25 30	

atg act gga ttc cca gtg aag aag gtc aac act gac att act tcc att	144
Met Thr Gly Phe Pro Val Lys Lys Val Asn Thr Asp Ile Thr Ser Ile	
35 40 45	

aca agc aat ggt gga aga gta aag tgc atg cag gtg tgg cct cca att	192
Thr Ser Asn Gly Gly Arg Val Lys Cys Met Gln Val Trp Pro Pro Ile	
50 55 60	

gga aag aag aag ttt gag act ctt tcc tat ttg cca cca ttg acc aga	240
Gly Lys Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg	
65 70 75 80	

gat tcc cgg gtg agg cca gaa atc gct gta ctt gat atc caa ggt cag	288
Asp Ser Arg Val Arg Pro Glu Ile Ala Val Leu Asp Ile Gln Gly Gln	
85 90 95	

tat cgg gtt tac acg gag ttc tat cgc gcg gat gcg gcc gaa aac acg	336
Tyr Arg Val Tyr Thr Glu Phe Tyr Arg Ala Asp Ala Ala Glu Asn Thr	
100 105 110	

atc atc ctg atc aac ggc tcg ctg gcc acc acg gcc tcg ttc gcc cag	384
Ile Ile Leu Ile Asn Gly Ser Leu Ala Thr Thr Ala Ser Phe Ala Gln	
115 120 125	

acg gta cgt aac ctg cac cca cag ttc aac gtg gtt ctg ttc gac cag	432
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Thr	Val	Arg	Asn	Leu	His	Pro	Gln	Phe	Asn	Val	Val	Leu	Phe	Asp	Gln	
130						135					140					
ccg	tat	tca	ggc	aag	tcc	aag	ccg	cac	aac	cgt	cag	gaa	cgg	ctg	atc	480
Pro	Tyr	Ser	Gly	Lys	Ser	Lys	Pro	His	Asn	Arg	Gln	Glu	Arg	Leu	Ile	
145					150					155					160	
agc	aag	gag	acc	gag	gcg	cat	atc	ctc	ctt	gag	ctg	atc	gag	cac	ttc	528
Ser	Lys	Glu	Thr	Glu	Ala	His	Ile	Leu	Leu	Glu	Leu	Ile	Glu	His	Phe	
				165					170					175		
cag	gca	gac	cac	gtg	atg	tct	ttt	tcg	tgg	ggc	ggc	gca	agc	acg	ctg	576
Gln	Ala	Asp	His	Val	Met	Ser	Phe	Ser	Trp	Gly	Gly	Ala	Ser	Thr	Leu	
			180					185					190			
ctg	gcg	ctg	gcg	cac	cag	ccg	ccg	tac	gtg	aag	aag	gca	gtg	gtg	agt	624
Leu	Ala	Leu	Ala	His	Gln	Pro	Arg	Tyr	Val	Lys	Lys	Ala	Val	Val	Ser	
		195					200					205				
tcg	ttc	tcg	cca	gtg	atc	aac	gag	ccg	atg	cgc	gac	tat	ctg	gac	cgt	672
Ser	Phe	Ser	Pro	Val	Ile	Asn	Glu	Pro	Met	Arg	Asp	Tyr	Leu	Asp	Arg	
	210					215					220					
ggc	tgc	cag	tac	ctg	gcc	gcc	tgc	gac	cgt	tat	cag	gtc	ggc	aac	ctg	720
Gly	Cys	Gln	Tyr	Leu	Ala	Ala	Cys	Asp	Arg	Tyr	Gln	Val	Gly	Asn	Leu	
225					230					235					240	
gtc	aat	gac	acc	atc	ggc	aag	cac	ttg	ccg	tcg	ctg	ttc	aaa	cgc	ttc	768
Val	Asn	Asp	Thr	Ile	Gly	Lys	His	Leu	Pro	Ser	Leu	Phe	Lys	Arg	Phe	
				245					250					255		
aac	tac	cgc	cat	gtg	agc	agc	ctg	gac	agc	cac	gag	tac	gca	cag	atg	816
Asn	Tyr	Arg	His	Val	Ser	Ser	Leu	Asp	Ser	His	Glu	Tyr	Ala	Gln	Met	
			260					265					270			
cac	ttc	cac	atc	aac	cag	gtg	ctg	gag	cac	gac	ctg	gaa	cgt	gcg	ctg	864
His	Phe	His	Ile	Asn	Gln	Val	Leu	Glu	His	Asp	Leu	Glu	Arg	Ala	Leu	
		275					280					285				
caa	ggc	gcg	cgc	aat	atc	aac	atc	ccg	gtg	ctg	ttc	atc	aac	ggc	gag	912
Gln	Gly	Ala	Arg	Asn	Ile	Asn	Ile	Pro	Val	Leu	Phe	Ile	Asn	Gly	Glu	
	290					295					300					
cgc	gac	gag	tac	acc	aca	gtc	gag	gat	gcg	cgg	cag	ttc	agc	aag	cat	960
Arg	Asp	Glu	Tyr	Thr	Thr	Val	Glu	Asp	Ala	Arg	Gln	Phe	Ser	Lys	His	
305					310					315					320	
gtg	ggc	aga	agc	cag	ttc	agc	gtg	atc	cgc	gat	gcg	ggc	cac	ttc	ctg	1008
Val	Gly	Arg	Ser	Gln	Phe	Ser	Val	Ile	Arg	Asp	Ala	Gly	His	Phe	Leu	
				325					330				335			
gac	atg	gag	aac	aag	acc	gcc	tgc	gag	aac	acc	cgc	aat	gtc	atg	ctg	1056
Asp	Met	Glu	Asn	Lys	Thr	Ala	Cys	Glu	Asn	Thr	Arg	Asn	Val	Met	Leu	
			340					345					350			

ggc ttc ctc aag cca acc gtg cgt gaa ccc cgc caa cgt tac caa ccc 1104  
Gly Phe Leu Lys Pro Thr Val Arg Glu Pro Arg Gln Arg Tyr Gln Pro  
355 360 365

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gtg cag cag ggg cag cat gca ttt gcc atc tga      1137
Val Gln Gln Gly Gln His Ala Phe Ala Ile
      370              375

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<210> 29

<211> 378

<212> PRT

<213> Pseudomonas putida

<400> 29

Met Ala Ser Met Ile Ser Ser Ser Ala Val Thr Thr Val Ser Arg Ala  
1 5 10 15

Ser Arg Gly Gln Ser Ala Ala Met Ala Pro Phe Gly Gly Leu Lys Ser  
20 25 30

Met Thr Gly Phe Pro Val Lys Lys Val Asn Thr Asp Ile Thr Ser Ile  
35 40 45

Thr Ser Asn Gly Gly Arg Val Lys Cys Met Gln Val Trp Pro Pro Ile  
50 55 60

Gly Lys Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg  
65 70 75 80

Asp Ser Arg Val Arg Pro Glu Ile Ala Val Leu Asp Ile Gln Gly Gln  
85 90 95

Tyr Arg Val Tyr Thr Glu Phe Tyr Arg Ala Asp Ala Ala Glu Asn Thr  
100 105 110

Ile Ile Leu Ile Asn Gly Ser Leu Ala Thr Thr Ala Ser Phe Ala Gln  
115 120 125

Thr Val Arg Asn Leu His Pro Gln Phe Asn Val Val Leu Phe Asp Gln  
 130 135 140

Pro Tyr Ser Gly Lys Ser Lys Pro His Asn Arg Gln Glu Arg Leu Ile  
 145 150 155 160

Ser Lys Glu Thr Glu Ala His Ile Leu Leu Glu Leu Ile Glu His Phe  
 165 170 175

Gln Ala Asp His Val Met Ser Phe Ser Trp Gly Gly Ala Ser Thr Leu  
 180 185 190

Leu Ala Leu Ala His Gln Pro Arg Tyr Val Lys Lys Ala Val Val Ser  
 195 200 205

Ser Phe Ser Pro Val Ile Asn Glu Pro Met Arg Asp Tyr Leu Asp Arg  
 210 215 220

Gly Cys Gln Tyr Leu Ala Ala Cys Asp Arg Tyr Gln Val Gly Asn Leu  
 225 230 235 240

Val Asn Asp Thr Ile Gly Lys His Leu Pro Ser Leu Phe Lys Arg Phe  
 245 250 255

Asn Tyr Arg His Val Ser Ser Leu Asp Ser His Glu Tyr Ala Gln Met  
 260 265 270

His Phe His Ile Asn Gln Val Leu Glu His Asp Leu Glu Arg Ala Leu  
 275 280 285

Gln Gly Ala Arg Asn Ile Asn Ile Pro Val Leu Phe Ile Asn Gly Glu  
 290 295 300

Arg Asp Glu Tyr Thr Thr Val Glu Asp Ala Arg Gln Phe Ser Lys His  
 305 310 315 320

Val Gly Arg Ser Gln Phe Ser Val Ile Arg Asp Ala Gly His Phe Leu  
 325 330 335

Asp Met Glu Asn Lys Thr Ala Cys Glu Asn Thr Arg Asn Val Met Leu  
 340 345 350

Gly Phe Leu Lys Pro Thr Val Arg Glu Pro Arg Gln Arg Tyr Gln Pro  
           355                                  360                                  365

Val Gln Gln Gly Gln His Ala Phe Ala Ile  
       370                                  375

<210> 30

<211> 1149

<212> DNA

<213> Pseudomonas putida

<400> 30

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ggatccatgg cttctatgat atcctcttcc gctgtgacaa cagtcagccg tgcctctagg      60
gggcaatccg ccgcaatggc tccattcggc ggcctcaaatt ccatgactgg attcccagtg      120
aagaagggtca acactgacat tactttccatt acaagcaatg gtggaagagt aaagtgcattg      180
cagggtgtggc ctccaattgg aaagaagaag tttgagactc tttcctatatt gccaccattg      240
accagagatt cccgggtgag gccagaaatc gctgtacttg atatccaagg tcagtatcgg      300
gtttacacgg agttctatcg cgcggatgcg gccgaaaaca cgatcatcct gatcaacggc      360
tcgctggcca ccacggcctc gttcgcccag acggtacgta acctgcaccc acagttcaac      420
gtggttctgt tcgaccagcc gtattcaggc aagtccaagc cgacaaccg tcaggaacgg      480
ctgatcagca aggagaccga ggcgcataatc ctcttgagc tgatcgagca cttccaggca      540
gaccacgtga tgtctttttc gtgggggtggc gcaagcacgc tgctggcgct ggcgaccag      600
ccgcggtacg tgaagaaggc agtgggtgagt tcgttctcgc cagtgatcaa cgagccgatg      660
cgcgactatc tggaccgtgg ctgccagtac ctggccgcct gcgaccgtta tcaggtcggc      720
aacctgggtca atgacaccat cggcaagcac ttgccgtcgc tgttcaaacg cttcaactac      780
cgccatgtga gcagcctgga cagccacgag tacgcacaga tgcaattcca catcaaccag      840
gtgctggagc acgacctgga acgtgcgctg caaggcgcg cgaatatcaa catcccgggtg      900
ctgttcatca acggcgagcg cgacgagtag accacagtcg aggatgcgcg gcagttcagc      960
aagcatgtgg gcagaagcca gttcagcgtg atccgcgatg cgggccactt cctggacatg     1020

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gagaacaaga ccgcctgcga gaacacccgc aatgtcatgc tgggcttcct caagccaacc 1080  
 gtgcgtgaac cccgccaacg ttaccaaccc gtgcagcagg ggcagcatgc atttgccatc 1140  
 tgaggtacc 1149

<210> 31

<211> 519

<212> DNA

<213> *Aeromonas caviae*

<220>

<221> CDS

<222> (1)..(519)

<400> 31

atg agc gca caa tcc ctg gaa gta ggc cag aag gcc cgt ctc agc aag 48  
 Met Ser Ala Gln Ser Leu Glu Val Gly Gln Lys Ala Arg Leu Ser Lys  
 1 5 10 15

cgg ttc ggg gcg gcg gag gta gcc gcc ttc gcc gcg ctc tcg gag gac 96  
 Arg Phe Gly Ala Ala Glu Val Ala Ala Phe Ala Ala Leu Ser Glu Asp  
 20 25 30

ttc aac ccc ctg cac ctg gac ccg gcc ttc gcc gcc acc acg gcg ttc 144  
 Phe Asn Pro Leu His Leu Asp Pro Ala Phe Ala Ala Thr Thr Ala Phe  
 35 40 45

gag cgg ccc ata gtc cac ggc atg ctg ctc gcc agc ctc ttc tcc ggg 192  
 Glu Arg Pro Ile Val His Gly Met Leu Leu Ala Ser Leu Phe Ser Gly  
 50 55 60

ctg ctg ggc cag cag ttg ccg ggc aag ggg agc atc tat ctg ggt caa 240  
 Leu Leu Gly Gln Gln Leu Pro Gly Lys Gly Ser Ile Tyr Leu Gly Gln  
 65 70 75 80

agc ctc agc ttc aag ctg ccg gtc ttt gtc ggg gac gag gtg acg gcc 288  
 Ser Leu Ser Phe Lys Leu Pro Val Phe Val Gly Asp Glu Val Thr Ala  
 85 90 95

gag gtg gag gtg acc gcc ctt cgc gag gac aag ccc atc gcc acc ctg 336  
 Glu Val Glu Val Thr Ala Leu Arg Glu Asp Lys Pro Ile Ala Thr Leu  
 100 105 110

acc acc cgc atc ttc acc caa ggc ggc gcc ctg gcc gtg acg ggg gaa 384  
 Thr Thr Arg Ile Phe Thr Gln Gly Gly Ala Leu Ala Val Thr Gly Glu  
           115                  120                  125

gcc gtg gtc aag ctg cct tca aaa gct ttg ggc aaa ggt gtt acc gag 432  
 Ala Val Val Lys Leu Pro Ser Lys Ala Leu Gly Lys Gly Val Thr Glu  
           130                  135                  140

gaa caa ttc aaa gag acc tgg acg agg ccg gga gct gct gga atg ggc 480  
 Glu Gln Phe Lys Glu Thr Trp Thr Arg Pro Gly Ala Ala Gly Met Gly  
           145                  150                  155                  160

gaa ggg act agc ctt gtg gtg gcc aag tcc aga atg taa 519  
 Glu Gly Thr Ser Leu Val Val Ala Lys Ser Arg Met  
                           165                  170

<210> 32

<211> 172

<212> PRT

<213> *Aeromonas caviae*

<400> 32

Met Ser Ala Gln Ser Leu Glu Val Gly Gln Lys Ala Arg Leu Ser Lys  
 1                  5                  10                  15

Arg Phe Gly Ala Ala Glu Val Ala Ala Phe Ala Ala Leu Ser Glu Asp  
           20                  25                  30

Phe Asn Pro Leu His Leu Asp Pro Ala Phe Ala Ala Thr Thr Ala Phe  
           35                  40                  45

Glu Arg Pro Ile Val His Gly Met Leu Leu Ala Ser Leu Phe Ser Gly  
           50                  55                  60

Leu Leu Gly Gln Gln Leu Pro Gly Lys Gly Ser Ile Tyr Leu Gly Gln  
 65                  70                  75                  80

Ser Leu Ser Phe Lys Leu Pro Val Phe Val Gly Asp Glu Val Thr Ala  
           85                  90                  95

Glu Val Glu Val Thr Ala Leu Arg Glu Asp Lys Pro Ile Ala Thr Leu  
                   100                  105                  110

Thr Thr Arg Ile Phe Thr Gln Gly Gly Ala Leu Ala Val Thr Gly Glu  
           115                  120                  125

Ala Val Val Lys Leu Pro Ser Lys Ala Leu Gly Lys Gly Val Thr Glu  
       130                  135                  140

Glu Gln Phe Lys Glu Thr Trp Thr Arg Pro Gly Ala Ala Gly Met Gly  
   145                  150                  155                  160

Glu Gly Thr Ser Leu Val Val Ala Lys Ser Arg Met  
                   165                  170

<210> 33

<211> 598

<212> DNA

<213> *Aeromonas caviae*

<400> 33

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ggatccatga gcgcacaatc cctggaagta ggccagaagg cccgtctcag caagcgggttc      60
ggggcggcgg aggtagccgc cttcgccgcg ctctcgaggg acttcaaccc cctgcacctg      120
gaccggcctt tcgccgccac cacggcggtt gagcggccca tagtccacgg catgctgctc      180
gccagcctct tctccggggt gctgggccag cagttgccgg gcaaggggag catctatctg      240
gggtcaaagcc tcagcttcaa gctgccggtc tttgtcgggg acgaggtgac ggccgaggtg      300
gaggtgaccg cccttcgcga ggacaagccc atcgccaccc tgaccaccgg catcttcacc      360
caaggcggcg ccctcgccgt gacgggggaa gccgtgggtca agctgccttc aaaagctttg      420
ggcaaaggtg ttaccgagga acaattcaaa gagacctgga cgaggccggg agctgctgga      480
atgggcgaag ggcgaaggga ctagccttgt ggtggccaag tccagaatgt aagacagacg      540
ttcattgcgg cggagcggcc aaggcgggtt ggcattcttc cagaaaaaca actagggg      598

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<210> 34

<211> 31

<212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer TphaF

<221> misc\_feature  
 <222> 1, 2, 3, 4, 5, 6  
 <223> n = A,T,C or G

<400> 34  
 nnnnnnggat ccatggcttc tatgatatcc t

31

<210> 35  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer PhaF

<221> misc\_feature  
 <222> 1, 2, 3, 4, 5, 6  
 <223> n = A,T,C or G

<400> 35  
 nnnnnnggat ccatgactga cgttgatcatc

30

<210> 36  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer PhbF

<221> misc\_feature  
 <222> 1, 2, 3, 4, 5, 6  
 <223> n = A,T,C or G

<400> 36  
 nnnnnnggat ccatgactca gcgcattgcg

30

<210> 37  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer PhcF

<221> misc\_feature  
 <222> 1, 2, 3, 4, 5, 6

<223> n = A,T,C or G

<400> 37  
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<210> 38  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer PhaR

<400> 38  
ctgagtcatg tccactcc 18

<210> 39  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer PhbR

<400> 39  
ctgccgactg gtggaacc 18

<210> 40  
<211> 18  
<212> DNA  
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<220>  
<223> PCR primer PhcR

<400> 40  
gaagcgtcat gccttggc 18

<210> 41  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer PhaClCf

<221> misc\_feature  
<222> 1, 2, 3, 4, 5, 6  
<223> n = A,T,C or G

<400> 41  
nnnnnnggat ccatgagcca gaagaac 27

<210> 42

<211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer PhaC1Cr

<221> misc\_feature  
 <222> 1, 2, 3, 4, 5, 6  
 <223> n = A,T,C or G

<400> 42  
 nnnnnnggta cctcatcggt catgcacg

28

<210> 43  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer PhaC1Pf

<221> misc\_feature  
 <222> 1, 2, 3, 4, 5, 6  
 <223> n = A,T,C or G

<400> 43  
 nnnnnncccg ggtgagccag aagaacaata ac

32

<210> 44  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer PhaJF

<400> 44  
 ggatccatga gcgcacaatc cctgg

25

<210> 45  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer PhaJR

<400> 45  
 aagcttttga aggcagcttg accacgg

27

<210> 46  
 <211> 27  
 <212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer PhaGF

<400> 46

cccgggtgag gccagaaatc gctgtac

27

<210> 47

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer PhaGR

<400> 47

ggtacctcag atggcaaag catgc

25

<210> 48

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer SSP-F

<221> misc\_feature

<222> 1, 2

<223> n = A,T,C or G

<400> 48

nngagctcga tgggaggtgc tcgaagacat attacc

36

<210> 49

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer SSP-R

<221> misc\_feature

<222> 1, 2

<223> n = A,T,C or G

<400> 49

nnggatcctg tactagatat ggcagc

26

<210> 50

<211> 38

<212> DNA

<213> Artificial Sequence

<220>  
 <223> PCR primer 3  
  
 <400> 50  
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 <210> 51  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> PCR primer 4  
  
 <400> 51  
 catcttactg gtaccttttag tacaacggtg acgcc 35  
  
 <210> 52  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> PCR primer 5  
  
 <400> 52  
 ctactcattt actagtcacc atgagcacat acgaaggtc 39  
  
 <210> 53  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> PCR primer 6  
  
 <400> 53  
 catcttactg gtaccttcag cgtttatacg cttgca 36  
  
 <210> 54  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> PCR primer 1  
  
 <400> 54  
 ctactcataa ccatggcgcc caccgtg 27  
  
 <210> 55  
 <211> 43  
 <212> DNA



<213> Artificial Sequence

<220>

<223> PCR primer 2

<400> 55

catcttactc atatgccgca cctgcatgca ccggatcctt ccg

43

<210> 56

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Five extra N-terminal amino acid residues in a CPL  
variant

<400> 56

Met Gln Val Arg His

1

5